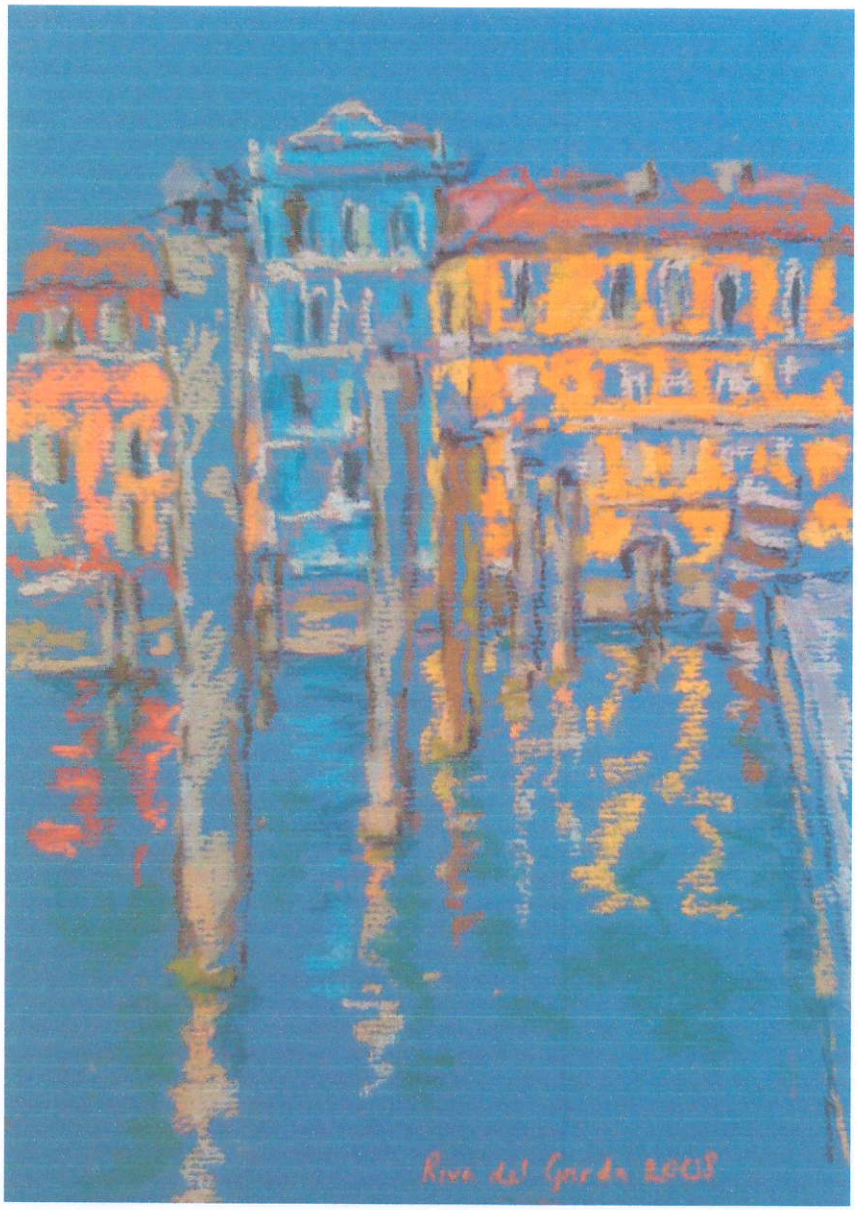

52nd Annual Maize Genetics Conference

Program and Abstracts

March 18 – March 21, 2010

Congress Centre
Riva del Garda (Trento), Italy

P229

QTL mapping for root characteristics at the seedling stage in maize

(submitted by silvia giuliani <silgiul27@yahoo.com>)
Full Author List: Giuliani, Silvia[1]; Busatto, Carla[1]; Salvi, Silvio[1]; Claudia, Ricciolini[1]; Carraro, Nicola[1]; Presterl, Thomas[2]; Ouzunova, Milena[2]; Sanguineti, Maria Corinna[1]; Tuberosa, Roberto[1]
[1] Department of Agroenviromental Sciences and Technologies, University of Bologna, Viale Fanin 44, 40127 Bologna, Italy
[2] KWS SAAT AG, Maize Breeding, Einbeck, Germany

In order to elucidate the genetic control of root architecture in maize, a collection of maize introgression library (IL) lines developed from the cross between two parents contrasting for root traits (B73 and Gaspé Flint) was studied. The IL collection includes 75 lines, most of which retain one single chromosome introgression of the donor genome (Gaspé Flint) of an average length of ca. 40 cM. It has been estimated that ca. 70% of the Gaspé Flint genome is represented within the collection. The IL lines were evaluated for root characteristics by applying two different methodologies, i.e. a paper-roll based protocol and a pot-growing system (seedlings grown until the fourth-leaf stage in sand/clay pebble pots). Particularly striking differences were observed between the two parental lines and among the IL lines for the number of seminal roots developing from the scutellar node. B73 produced an average of 2.8 seminal roots per plant while Gaspé Flint did not develop any seminal root. Among the IL lines, a few showed a Gaspé-like phenotype for seminal root number, implying that the QTLs controlling this trait are localized on the corresponding introgressions. A major QTL for number of seminal roots (*Seminal root 1, Sr1*) was localized on chromosome 1S, ca. 10-15 cM away from the root architecture locus *Rtcs1* (Taramino et al., 2007, Plant J. 50:649-659). Phenotypic expression and fine genetic mapping data seem to indicate that the two loci do not coincide. Positional cloning of *Sr1* is underway.

P230

QTLs and genes for Mediterranean corn borer resistance

(submitted by Rosa Ana Malvar <rmalvar@mbg.cesga.es>)
Full Author List: Malvar, Rosa Ana[1]; Ordás, Bernardo[1]; Santiago, Rogelio[1]; Butrón, Ana[1]
[1] Misión Biológica de Galicia CSIC, Apartado 28, Pontevedra, Spain, 36080

Ostrinia nubilalis (ECB) and *Sesamia nonagrioides* (MCB) cause important losses in temperate maize production as a consequence of stalk tunneling, but QTL analyses for resistance to stalk tunneling were mostly restricted to ECB. RIL populations derived from B73 × Mo17 and EP42 × EP39 were used to detect QTLs for resistance to stem tunneling by MCB. We detected two QTL at bins 1.06 and 9.04 with additive effects of approximately 4 cm of tunnel length in the B73 × Mo17 RIL population, and those QTLs were close to QTLs found previously for ECB resistance. Three QTLs were detected for stalk tunnel length at bins 1.02, 3.05 and 8.05 in the EP42 × EP39 RIL population. The QTLs at bin 3.05 and 8.05 were co-located to a QTL for plant height and grain humidity, and to a QTL for yield, respectively. Now, we will try to identify the resistance gene behind the QTL at bin 9.04 because the same region has been consistently associated to corn borer resistance in other populations. We have chosen one candidate gene, GRMZM2G116452, which encodes a peroxidase precursor. The possible relationship between polymorphisms at this gene and resistance to corn borers will be studied using a panel of 282 inbred lines which represent most of the genetic diversity of public inbred lines. The seed of the inbred lines and the genotypic data are available within the PANZEA project (http://www.panzea.org/lit/germplasma.html). On the other hand, we propose to do fine mapping with near-isogenic lines in the region 8.05 in which we have detected a QTL for resistance and yield. The objective will be to know if there is a QTL with pleiotropic effects on both characters or the effects are due to two linked QTLs.

Funding acknowledgement: National Plan for Research and Development of Spain (Projects Cod. AGL2006-13140, AGL 2009-09611)